

```

1  GCCCTTGGCA GCAGCCCTGT TACCGCTTAG ATGGCGCGCA GGACAGAGCC
51  CCCCACGGG GGCCTGGGGAC GGGTGGTGGT GCTCTCAGCG TTCTTCCAGT
101 CGGCGCTTGT GTTTGGGGTG CTCCGCTCCT TTGGGGTCTT CTTCGTGGAG
151 TTTGTGGCGG CGTTTGAGGA GCAGGCAGCG CGCGTCTCCT GGATCGCCTC
201 CATAGGAATC GCGGTGCAGC AGTTTGGGAG CCCGGTAGGC AGTGCCCTGA
251 GCACGAAGTT CGGGCCCAGG CCCGTGGTGA TGA CTGGAGG CATCTTGGCT
301 GCGCTGGGGA TGCTGCTCGC CTCTTTTGCT ACTTCTTGA CCCACCTATA
351 CCTGAGTATT GGGTTGCTGT CAGGCTCTGG CTGGGCTTTG ACCTTCGCTC
401 CGACCCTGGC CTGCCTGTCC TGTATTCT CTGCGCGACG ATCCCTGGCC
451 ACCGGGCTGG CACTGACAGG CGTGGGCCTC TCCTCCTTCA CATTTGCCCC
501 CTTTTTCCAG TGGCTGCTCA GCCACTACGC CTGGAGGGGG TCCCTGCTGC
551 TGGTGTCTGC TCTCTCCCTC CACCTAGTGG CCTGTGGTGC TCTCCTCCGC
601 CCACCTCTCC TGGCTGAGGA CCCTGCTGTG GGTGGTCCCA GGGCCCACT
651 CACCTCTCTC CTCCATCATG GCCCCTTCCT CCGTTACACT GTTGCCCTCA
701 CCCTGATCAA CACTGGCTAC TTCATTCCCT ACCTCCACCT GGTGGCCCAT
751 CTCCAGGACC TGGATTGGGA CCCACTACCT GCCGCCTTCC TACTCTCAGT
801 TGTTGCTATT TCTGACCTCG TGGGGCGTGT GGTCTCCGGA TGGCTGGGAG
851 ATGCAGTCCC AGGGCCTGTG ACACGACTCC TGATGCTCTG GACCACCTTG
901 ACTGGGGTGT CACTAGCCCT GTTCCCTGTA GCTCAGGCTC CCACAGCCCT
951 GGTGGCTCTG GCTGTGGCCT ACGGCTTCAC ATCAGGGGCT CTGGCCCCAC
1001 TGGCCTTCTC TGTGCTGCCT GAACTAATAG GGACTAGAAG GATTTACTGT
1051 GGCCTGGGAC TGTTGCAGAT GATAGAGAGC ATCGGGGGGC TGCTGGGGCC
1101 TCCTCTCTCA GGCTACCTCC GGGATGTGTC AGGCAACTAC ACGGCTTCTT
1151 TTGTGGTGGC TGGGGCCTTC CTTCCTTTCAG GGAGTGGCAT TCTCCTCACC
1201 CTGCCCCACT TCTTCTGCTT CTCAACTACT ACCTCCGGGC CTCAGGACCT
1251 TGTAACAGAA GCACTAGATA CTAAAGTTCC CCTACCCAAG GAGGGGCTGG
1301 AAGGAGGACT GAACTCCACA GAGTCAGGCC CAGAAAGCCA AAGCTTGACA
1351 GCTCCAGGTC TTCTCTTGCC ACGTCTTGGT CTCCACAGAA CCACAGTGCC
1401 TTAAGATTCT TGATCTGCCT CCCCCTAGAG CAGGCCTGGG GCTCCTGCAA
1451 TGTGTGTGCC AACCCTTT (SEQ ID NO:1)

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# **FEATURES:**

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5'UTR:      1-30
Start Codon: 31
Stop Codon: 1402
3'UTR:      1405

```

# **HOMOLOGOUS PROTEINS:**

## Top 10 BLAST Hits:

	Score	E
CRA 103000001515981 /altid=gi 7670446 /def=dbj BAA95074.1  (ABO...	250	3e-65
CRA 150000165029756 /altid=gi 13431667 /def=sp O70461 MOT3_RAT ...	244	1e-63
CRA 89000000192725 /altid=gi 10048452 /def=ref NP_065262.1  sol...	238	8e-62
CRA 18000005042369 /altid=gi 2497855 /def=sp Q63344 MOT2_RAT MO...	238	1e-61
CRA 18000005039313 /altid=gi 1432167 /def=gb AAB04023.1  (U6231...	238	1e-61
CRA 18000005141743 /altid=gi 6755536 /def=ref NP_035521.1  solu...	234	2e-60
CRA 335001098681302 /altid=gi 11418102 /def=ref XP_009979.1  mo...	234	2e-60
CRA 1000682335761 /altid=gi 7019529 /def=ref NP_037488.1  monoc...	233	5e-60
CRA 18000005141744 /altid=gi 4759120 /def=ref NP_004722.1  solu...	232	6e-60
CRA 108000024650708 /altid=gi 12737028 /def=ref XP_012127.1  so...	232	6e-60

## BLAST dbEST hits:

	Score	E
gi 8423571 /dataset=dbest /taxon=960...	733	0.0

# **EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hits:

gi|8423571 breast

From tissue screening panels:

Spleen

Breast (adult)

```

1 MARRTEPPDG GWGRVVLSA FFQSALVFGV LRSFGVFFVE FVAAFEEQAA
51 RVSWIASIGI AVQQFGSPVG SALSTKFGPR PVVMTGGILA ALGMLLASFA
101 TSLTHLYLSI GLLSGSGWAL TFAPTLACLS CYFSRRRSLA TGLALTGVGL
151 SSFTFAPFFQ WLLSHYAWRG SLLLVSALS HLVAACGALLR PPSLAEDPAV
201 GGPRAQLTSL LHHGFPLRYT VALTLINTGY FIPYLHLVAH LQDLWDWPLP
251 AAFLLSVVAI SDLVGRVVSG WLGDVPGPV TRLLMLWTTL TGVSLALFPV
301 AQAPTALVAL AVAYGFTSGA LAPLAFSVLP ELIGTRRIYC GLGLLQMIES
351 IGGLLGPPLS GYLDRVSGNY TASFVVAGAF LLSGSGILLT LPHFFCFSTT
401 TSGPQDLVTE ALDTKVPLPK EGLEGGLNST ESGPESQSLT APGLLLPRLG
451 LHRTTVP (SEQ ID NO:2)

```

# FEATURES:

## Functional domains and key regions:

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

Number of matches: 2

1	369-372 NYTA
2	428-431 NSTE

[2] PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE  
cAMP- and cGMP-dependent protein kinase phosphorylation site

135-138 RRRS

[3] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 3

1	74-76 STK
2	134-136 SRR
3	335-337 TRR

[4] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 2

1	193-196 SLAE
2	432-435 SGPE

[5] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 18

1	29-34 GVLRSF
2	66-71 GSPVGS
3	70-75 GSALST
4	86-91 GGILAA
5	87-92 GILAAL
6	93-98 GMLLAS
7	111-116 GLLSGS
8	115-120 GSGWAL
9	142-147 GLALTG
10	147-152 GVGLSS
11	201-206 GGPRAQ
12	292-297 GVSLAL
13	368-373 GNYTAS
14	386-391 GILLTL
15	422-427 GLEGGL
16	425-430 GGLNST
17	426-431 GLNSTE
18	450-455 GLHRTT

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	13	33	1.302	Certain
2	52	72	1.039	Certain
3	81	101	2.101	Certain
4	114	134	1.703	Certain
5	139	159	1.850	Certain
6	170	190	1.572	Certain
7	219	239	1.192	Certain
8	245	265	1.019	Certain
9	283	303	1.832	Certain
10	306	326	1.709	Certain
11	338	358	0.976	Putative
12	372	392	1.982	Certain

Membrane spanning structure and domains:

**BLAST Alignment to Top Hit:**

>CRA|150000165029756 /altid=gi|13431667 /def=sp|O70461|MOT3\_RAT  
 MONOCARBOXYLATE TRANSPORTER 3 (MCT 3) /org=MCT 3  
 /dataset=nraa /length=492  
 Length = 492

Score = 244 bits (617), Expect = 1e-63  
 Identities = 168/470 (35%), Positives = 239/470 (50%), Gaps = 36/470 (7%)

Query: 3 RRTEPPDGGWGRVVVLSAFFQSALVFGVLRSGVFFVEFVAAFEEQAARVSWIASIGIAV 62  
 R PPDGGWG VV+ + F + +G ++ VFF E F + +W++SI +A+  
 Sbjct: 8 RGAGPPDGGWGWVVLGACFVITGFAYGFPKAVSVFFRELKRDFGAGYSDTAWVSSIMLAM 67

Query: 63 QQFGSPVGSALSTKFGPRPVMTGGILAALGMLLASFATSLTHLYLSIGLLSGSGWALTF 122  
 P+ S L T+FG RPV++ GG+LA+ GM+LASFA+ L LYL+ G+L+G G AL F  
 Sbjct: 68 LYGTGPLSSILVTRFGCRPVMLAGLLASAGMILASFASRLLELYLTAGVLTGLGLALNF 127

Query: 123 APTLACLSCYFSRRRSLATGLALTGVGLSSFTFAPFFQWLLSHYAWRGSLLLVSALS LHL 182  
 P+L L YF RRR LA GLA G + T +P Q L + WRG LL L LH  
 Sbjct: 128 QPSLIMLGlyFERRRPLANGLAAAGSPVFLSTLSPLGQLGERFGWRGGFLLFGGLLLHC 187

Query: 183 VACGALLRPPSLAE---DPAVGGPRAQLTSLH-----HGPFLRYTVALTLINTGYFIPY 234  
 ACGA++RPP + DPA G RA+ LL F+ Y V L+ G F+P  
 Sbjct: 188 CACGAVMRPPPGPQPRPDAPPGGRARHRQLDLAVCTDRTFMVYMTKFLMALGLFVPA 247

Query: 235 LHLVAHLQDLDWDLPLPAAFLLSVVAISDLVGRVVGWLG--DAVPGPVTRLLMLWTTLTG 292  
 + LV + +D AAFLLS+V D+V R G L + V L L G  
 Sbjct: 248 ILLVNYAKDAGVPDAEAAFLLSIVGFVDIVARFACGALAGLGRLRPHVPYLFSLALLANG 307

Query: 293 VSLALFPVAQAPTALVALAVAYGFTSGALAPLAFSVLPELIGTRRIYCGLLQMIESIG 352  
 ++ + A++ LVA +A+G + G + L F VL +G R LGL+ ++E++  
 Sbjct: 308 LTDLISARARSYGLVAFICIAFGLSYGMVGALQFEVLMATVGAPRFPSPALGLVLLVEAVA 367

Query: 353 GLLGPPLSGYL RDVSGNYTASFVVGAFLLSGSGILLTLPHFFCFSTT----- 400  
 L+GPP +G L D NY F +AG+ ++ +G+ + + + C +  
 Sbjct: 368 VLIGPPSAGRLVDALKNYEIIIFYLAGS-EVALAGVFMVTTYCCLRCSKNISSGRSAEGG 426

Query: 401 TSGPQDLVTEALDTKVPLPKEGLEGGLNSTESGPESQSLTAPGLLLPRLG 450  
 S P+D+ EA P+P STE E SL A +L PR G  
 Sbjct: 427 ASDPEDV--EAERDSEMPA-----STE---EPGSLEALEVLSPRAG 463 (SEQ ID  
 NO:4)

>CRA|89000000192725 /altid=gi|10048452 /def=ref|NP\_065262.1| solute  
 carrier family 16 (monocarboxylic acid transporters),  
 member 8; proton-coupled monocarboxylate transporter 3  
 gene; proton-coupled monocarboxylate transporter 3 [Mus  
 musculus] /org=Mus musculus /taxon=10090 /dataset=nraa  
 /length=492  
 Length = 492

Score = 238 bits (602), Expect = 8e-62  
 Identities = 165/470 (35%), Positives = 236/470 (50%), Gaps = 36/470 (7%)

Query: 3 RRTEPPDGGWGRVVVLSAFFQSALVFGVLRSGVFFVEFVAAFEEQAARVSWIASIGIAV 62  
 R PPDGGWG VV+ + F + +G ++ VFF E F + +W++SI +A+  
 Sbjct: 8 RGAGPPDGGWGWVVLGACFVVTGFAYGFPKAVSVFFRELKRDFGAGYSDTAWVSSIMLAM 67

Query: 63 QQFGSPVGSALSTKFGPRPVMTGGILAALGMLLASFATSLTHLYLSIGLLSGSGWALTF 122  
 P+ S L T+FG RPV++ GG+LA+ GM+LASFA+ L LYL+ G+L+G G AL F  
 Sbjct: 68 LYGTGPLSSILVTRFGCRPVMLAGLLASAGMILASFASRLVELYLTAGVLTGLGLALNF 127

Query: 123 APTLACLSCYFSRRRSLATGLALTGVGLSSFTFAPFFQWLLSHYAWRGSLLLVSALS LHL 182  
P+L L YF RRR LA GLA G + +P Q L + WRG LL L LH  
Sbjct: 128 QPSLIMLGlyFERRRPLANGLAAAGSPVFLSMLSPLGQLLGERFGWRGGFLLFGGLLLHC 187

Query: 183 VACGALLRP---PSLAEDPAVGGPRAQLTSLH-----HGPFLRYTVALTLINTGYFIPY 234  
ACGA++RP P DP+ G A+ LL F+ Y V L+ G F+P  
Sbjct: 188 CACGAVMRPPPGPPRRDPSPHGGPARRRRLLDVAVCTDRAFVVYVVTKFLMALGLFVPA 247

Query: 235 LHLVAHLQDLWDPLPAAFLLSVVAISDLVGRVVSGLG--DAVPGPVTRLLMLWTTLTG 292  
+ LV + +D AAFLLS+V D+V R G L + V L L G  
Sbjct: 248 ILLVNYAKDAGVPDAEAAFLLSIVGFVDIVARPACGALAGLGRLRPHVPYLFSLALLANG 307

Query: 293 VSLALFPVAQAPTALVALAVAYGFTSGALAPLAFSVLPELIGTRRIYCGLLQMIESIG 352  
++ + A++ LVA +A+G + G + L F VL +G R LGL+ ++E++  
Sbjct: 308 LTDLISARARSYGTLVAFCIAFGLSYGMVGALQFEVLMATVGAPRFPSALGLVLLVEAVA 367

Query: 353 GLLGPPLSGYL RDVSGNYTASFVVGAFLLSGSGILLTLPHFFCFSTT----- 400  
L+GPP +G L D NY F +AG+ ++ +G+ + + + C +  
Sbjct: 368 VLIGPPSAGRLVDALKNYEIIIFLAGS-EVALAGVFMATVTTYCCLRCSKNISSGRSAEGG 426

Query: 401 TSGPQDLVTEALDTKVPLPKEGLEGGLNSTESGPESQSLTAPGLLLPRLG 450  
S P+D+ EA P+P STE E SL A +L PR G  
Sbjct: 427 ASDPEDV--EAERDSEMPA-----STE---EPGSLEALEVLSPRAG 463 (SEQ ID NO:5)

# Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF01587	Monocarboxylate transporter	204.9	1.2e-57	2
PF01925	Domain of unknown function	4.4	4.6	1
PF00348	Polyprenyl synthetases	3.7	6.1	1
PF00083	Sugar (and other) transporter	3.0	3.8	1
PF01306	LacY proton/sugar symporter	2.7	6.6	1
PF01309	Equine arteritis virus small envelope glycop	2.3	5	1

## Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF01925	1/1	65	97 ..	165	201 .]	4.4	4.6
PF00083	1/1	12	108 ..	1	113 [.]	3.0	3.8
PF01309	1/1	153	173 ..	1	21 [.]	2.3	5
PF00348	1/1	174	191 ..	1	19 [.]	3.7	6.1
PF01587	1/2	20	192 ..	1	191 [.]	160.8	2.3e-44
PF01587	2/2	219	377 ..	441	611 .]	48.3	1.6e-12
PF01306	1/1	373	393 ..	393	415 .]	2.7	6.6

1 CATTTTTAGT GCATGGATTT TCTAACTGAA CCCCTTGGGC AACGCTTAAT  
 51 AGTAGGTACT ATTATCCCCA GTTTACAGAT GGGGAAACCA ACTGAGAGAT  
 101 TCAGCATCTT GATCGAGTTA AGTAATAAAG TCAAGATTGG AACTGGGCCA  
 151 GGCACGGTGG CTCACGCCTG TAATCCCAGC ACTTTGGGAG GCCAAGGCTG  
 201 GTGGATCACT TGAGGTCAGG AGTTCGAGAC CAGCGTGGCC AACATGGTGA  
 251 GACCTCGTCT CTACTAAAAA TACCAAAATT AACTGGGCGT TGTGGTGGGA  
 301 GCCTGTAATC CCAGAACTC AGGAGACTGA GGCAGGAGAA TCACTTGAAC  
 351 CCGGGAGGTG GAGGTTGCAG TGAGCCAAGA TCATGCCACT GCACTCCAGC  
 401 CTGGGCCACA GAGCAAGACT CCGTCTCAA AATAATAAAT AAATAAATAA  
 451 ATAAATAAAA GACTGGAAT GTGATCTGAT TCTAAAGACC CGAGTTCTTA  
 501 ATCACTATGT AATACAGCCA CAGCAATTTT TGTATCTTTG GCATATTCCC  
 551 CACCAGCCGA CATTTTGACT CTTAGAAAGT ATATATGTGT ATTATTGATG  
 601 ATTACTTTTA TTTCCACAT ATAAATTAT TTAAGGCTCA ATATGTCTTT  
 651 TAAGACTGCA CACCTCCCTC CCTGCCTCCA CTTCTTGTTT GCTGCTTTCC  
 701 CCAGTAATCT GGGAGTGAAC ATTGAGTCCA CGGTTTCAAG GTCAGGGTCC  
 751 TGGGAAGTAT GGCTTATAAT GAAGGAACAG GAAATCCAAG CCATTGGTGT  
 801 TATGGAGACT GGAAGGACT GGGGAGTGTT TGCTAGGGGC CTGAGGACTA  
 851 CTTGGGTAAG AGGGGGCTGA CTGCTCCAGT GGCCAGGGT ATAGTTTTGT  
 901 CTCTTTAGTC TACCCACCA TCAGATCAA AAAGGTGGT AGGAAGTGGT  
 951 TGTTACTAGA GGCAGAGGA AAAGGTTCCA GCCCAGTGA GGAAGAGGTA  
 1001 GGTGGTGTG GTGGGGCCCT GTGTGAGCTT ACAGCCGCC TCTCTCTCCT  
 1051 CAGTTATTTT TGGTCTCTGT GACCTGTAGG TTTCTGTTA GTGGGAACAG  
 1101 AAGTGACAGG AACGAGTTCC CACTACAGAA ATGAACGCCA GGAGTCCAAC  
 1151 TCATTCCCTT TCTCTCTTCC CTTAGCCGTT GAACTTCTCA GGGATCCAGG  
 1201 CTTCTAGGTC TGGCTGCCA GGGCTGCGTG TTAGTGGCTT CAGGCGCTGC  
 1251 GCCAAACACT TCGTTTGAAG CTCATCTCCT AACCCCTCCC CTACCCCAA  
 1301 CAGGGCCTTG CAATTCCTGG ACCCTCATT AAAGCAAGAG AGTCCTCTCC  
 1351 TCTCCAGACC CAGTTTACCC ACCACTAACC CTTCCGTGTG GCTCTGGGTG  
 1401 CTGAAACGGG GATGACTTGG CCCGCTAGGT GAAGAGGAGA CGGAAGCTTC  
 1451 CTGGCAGTCC CCGCGTCACG TGGGGCCCTA CCTAGTCAGC CTCCTAACGC  
 1501 CCCTCCTTAC GCATGCGCCC ATTCAGTGT GGTCCCCAAC AATGCCTAAA  
 1551 TCCCGCCCTG CCCTTCTCGT TCCGCCCCTG CCCGGGAGCC CCGCGTCTC  
 1601 ATTGGCGAGC TCCAGGGTGG CCCGGCCCGG ACACCCAGT GATAAAATAG  
 1651 ATCATCTACA CGGAACTGG CGCGCTCCAG GGGTGGGGCC CAACTCAGT  
 1701 TCCACCTCTT GGCTCCCAGC CGAACACCGA ACCGGGACCG ATCCGGCCCC  
 1751 GGCTTGAAGT AGCTCAGCTC CGAGCTCGCG GAACACGCC CCCGGGAGAC  
 1801 TCTGGCCCGG CCAGCGCGGG CCAGTCTTC AGTCTATAT CGCCCTGCCT  
 1851 TGGGAAAAGG TGCAGGGGCC TCTCGCCGCC TCGTCGGGCC CTTCTCTCT  
 1901 ACCTGCCTCT CCAACCCCTC TCGGCCCGA GCCACCGGC AGCGGGGTG  
 1951 GGTGTGCAGA GGTGCGGCGT CCAGAACCG GCTCCTGCAG AGGCTCTGGG  
 2001 TGGCAGCAGC CCTGTTACCG CTTAGATGGC GCGCAGGACA GAGCCCCCG  
 2051 ACGGGGGCTG GGGATGGGTG GTGGTGTCT CAGCGTTCTT CCAGTCGGCG  
 2101 CTTGTGTTTG GGTGCTCCG CTCCTTTGGG GTCTTCTTCG TGGAGTTTGT  
 2151 GCGGCGTTT GAGGAGCAGG CAGCGCGCGT CTCCTGGATC GCCTCCATAG  
 2201 GAATCGCGGT GCAGCAGTTT GGGAGTGAGT GCGGCGCTG GATCTGGCGG  
 2251 ACTGCGACCC TCGGAAGGGA GAGGGAATGC GCGACTGGG AAGTGAAGG  
 2301 GCGAGGGGCG GGAGATGCTG GGGGGGAGAC CCCTGAGATC TTCTCGCAGC  
 2351 GCCCTTCCA CTTCTCAGG CCCGCTAGGC AGTGCCCTGA GCACGAAGTT  
 2401 CGGGCCCAGG CCCGTGGTGA TGAAGGAGG CATCTTGGCT GCGCTGGGGA  
 2451 TGCTGCTCGC CTCTTTTGCT ACTTCCTTGA CCCACCTATA CCTGAGTATT  
 2501 GGGTTGCTGT CAGGTGAGAG CCTGCACAAG GGCAGGAGAG TCAAATGCTT  
 2551 AGATCGTTGG ATGTTACCT CTTCTCTGCT CTTTCCAAAG GGTTGGGGGA  
 2601 GAAGCTGAGG GAAAGTTTAG CTAGCACCTG TACCCAGAAG GGAATTCTTA  
 2651 ATAGGAATGA CTAAGCGAC AAACATGGTG AGGAATTAGG AAATTCAAGG  
 2701 ATGATGAAAC CTGGCCAGGC ACGGTGGCTC ACGCCTGTAA TCCCAGCACT  
 2751 TTGGGAAGCC GAGGCGGGTG GATCAGGAG TCAGGAGTTT GAGACCAGCC  
 2801 TGGCCAAACAT GGTGAAACCC CGTCTCTACA AAAATACAAA AATTAGCCCG  
 2851 GCCTGGTGGC GCTAATCCCA GTTACTCGGG AGGCTGAGGC AGGAGAATCG  
 2901 CTTGAACCCG GGAGGCGGAG GTTGCAGTGA GCCAAGATCG CACCACTGCA  
 2951 CTCCAGCCTG GCGGACAGAG CAAGATTCTG TCTCAAAAAA AAAAAAAAAA  
 3001 AAAAAAAAAA AGATGAAACC AAGTATACAA GCCCAGAAGC CTAGGGCTAA  
 3051 TGGGACTGGA GTGCAAAAGG AAGAATTACT ATAAATGGT GCTAGGGGCC  
 3101 AGGCACGGTG GCTCACGCC TGAATCCAG CACTTTGGGA GGCCGAGGCG

FIGURE 3, page 1 of 4

3151 GGGCGATCAC GAGGTCAGGA GATCAAGACC ATCCTGGCTA ACACGGTGAA  
3201 ATCACGTCTC TACTAAAAAC AAAAAAATT AGCTGGGCGT GGTGGCAGGT  
3251 GACTGTAGTC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA TGGTGTGAAC  
3301 CCGGGAAGCA GAGCTTGCAG TGAGCCGAGA TTGCACCACT GCACTCCAGC  
3351 CTGGGCGACA AAGTCGACT CCGTCTCAAA AAAAAAAGA AAAAAAAGG  
3401 TGCTAGGTAC TGTGACTGTG AAATCGATAT CATTATTGGA TTTACAGCTG  
3451 GGGAAAAGCT TTAAAGCTTA TACAACCTGG CAAATGAAGG TCACACAGCT  
3501 AGAAATGGTA GAGCCAGGT CTAACCTCAA AGTTCTGTGC TAGTTACCTT  
3551 ACAAACCTTG TCTCTAATCT TCCACAATCC CAAAAAGTGT ATTATTACAT  
3601 TTTGCAGTTG AGAAGGTTGA GGCTGGGGGT GTTAAGTAAA ACACACAAGG  
3651 TTACACAGCT ATGAAGTATC CAAGCCAAGA TTGTATCCCA GGTCTGTGGG  
3701 ACTCCGAAGC AAGTGCTACA TTCTGCTGCT GGGCAATGCG GGGATTACTG  
3751 TGTGCCTTGA GCTCCCTAAG AGTTCTCAAC ACCACTTCTT CCTTTTGTGAC  
3801 AGGCTCTGGC TGGGCTTTGA CCTTCGCTCC GACCCTGGCC TGCCTGTCTT  
3851 GTTATTTCTC TCGCCGACGA TCCCTGGCCA CCGGGCTGGC ACTGACAGGC  
3901 GTGGGCTCTT CCTCCTTCAC ATTTGCCCCC TTTTTCAGT GGCTGCTCAG  
3951 CCACTACGCC TGGAGGGGGT CCCTGCTGCT GGTGTCTGCC CTCTCCCTCC  
4001 ACCTAGTGGC CTGTGGTGCT CTCCTCCGCC CACCCTCCCT GGCTGAGGAC  
4051 CCTGCTGTGG GTGGTCCAG GGCCCAACTC ACCTCTCTCC TCCATCATGG  
4101 CCCCTTCCTC CGTTACACTG TTGCCCTCAC CCTGATCAAC ACTGGCTACT  
4151 TCATTCCCTA CCTCCACCTG GTGGCCCATC TCCAGGACCT GGATTGGGAC  
4201 CCACTACCTG CTGCCTTCCT ACTCTCAGT GTTGCTATTT CTGACCTCGT  
4251 GGGGCGTGTG GTCTCCGGAT GGCTGGGAGA TGCAGTCCCA GGGCCTGTGA  
4301 CACGACTCCT GATGCTCTGG ACCACCTTGA CTGGGGTGTC ACTAGCCCTG  
4351 TTCCCTGTAG CTCAGGCTCC CACAGCCCTG GTGGCTCTGG CTGTGGCCTA  
4401 CGGCTTCACA TCAGGGGGCTC TGGCCCCACT GGCCTTCTCT GTGCTGCCTG  
4451 AACTAATAGG GACTAGAAGG ATTTACTGTG GCCTGGGACT GTTGCGAGATG  
4501 ATAGAGAGCA TCGGGGGGCT GCTGGGGGCT CCTCTCTCAG GTAAGTGGAA  
4551 TGGGGTTCCC AGGGGGGTGAG GGCTGCCATG TTGCACAAC AGGGGAGGGT  
4601 ACTATTCTCA TTACAGTGA TGTGAATATT GCCCTCTGGT GTAGTACAGT  
4651 ACACAGCCTG CGTGCCCAAC CATAGCATCC CTGAAATGGG TCCATGGGGC  
4701 AAAGAACTTG GGGCTGGGAA AGTCTGAGTG GAAAGACAAA AAGAAGCTAA  
4751 GTGGAACCTT TGGCAGGGTG CCTACGGCTT GGGTTTGCAG AGGACCTGGC  
4801 AGAACCTGGC CAGACACAGA CGTAGCATTC CAGTGTGCAC CCTTTCCTTT  
4851 GGCTACTGAG GCCCCAAACC AGGTATCTGA GGCACCTGGT CAAAGTTCTG  
4901 CTGGCTCAGG GTGCCAGAAC TTTCAGACCT TTATCTCCTC TTACCCATTA  
4951 ACTGAAGCTT TAGAAAGGCC ACAGTTGGTG GGCCTCTGTA GTCCCAGCTA  
5001 CTCAGGAGGC TGAGGCAGGA GAATGGCATG AACCCGGGAG GCGGAGCTTG  
5051 CAGTGAGCTG AGATCGCGCC ACTGCACTTC AGCCTGGGCG ACAGAGCGAG  
5101 ACTCCGTCTC AAAAAAAGAA AAAAAAGAAA GGCCACAGTT GCCAGAAAGA  
5151 AAGGCACAAG TATGCCTGAC TCAATCTGGA TCTCCAAATC CCTGCAGGCT  
5201 GGTTTGGAGG TCCTTTCTGA AGGCGGGGAG GTGGTTGAAA TTAACCTTTG  
5251 AGGCCCTTTT GGGAAACCAG AGTTCTTAAG TTTATCCAAC TATTCCATGG  
5301 GAGTTCCAAC TCCTCTGAGA TGATAAGTCT TCCCTCCACC CAAAAATGTA  
5351 TCTGAGCCCT CAGCCCCAGC AAATAGATCA CTCATGTGTA TTCTTTTCTT  
5401 CTCTTGGACC TAGGCTACCT CCGGATGTG ACAGGCAACT ACACGGCTTC  
5451 TTTTGTGGTG GCTGGGGCCT TCCTTCTTTC AGGGAGTGGC ATTCTCCTCA  
5501 CCCTGCCCCA CTTCTTCTGC TTCTCAACTA CTACCTCCGG GCCCCAGGAC  
5551 CTTGTAACAG AAGCACTAGA TACTAAAGTT CCCCTACCCA AGGAGGGACT  
5601 GGAAGGAGGA CTGAACCTCA CAGAGTCAGG CCCAGAAAGC CAAAGCTTGA  
5651 CAGCTCCAGG TCTTCTCTTG CCACGTCTTG GTCTCCACAG AACCACAGTG  
5701 CCTTAAGATT CTTGATCTGC CTCCCCCTAG AGCAGGCCTG GGGCTCCTGC  
5751 AATGTGTGTG CCAACCCTTT GTATTTTGTG GAGGACTCTT ATTTCTCCGT  
5801 TACTCTCCTA ACCTTTTCTT CTTTTTCTT TTTCCCGAGA CGGAGTCTTG  
5851 CTCTGTGGCC CAGGCTGGAG TGCACTGATG TGATCTCGGC TCACTGCAAC  
5901 CTCCGCTTCC CGGGTTCAAG CGATTCTCCT GCCTCAGCCT CCCAAGTAGC  
5951 TGGGATTACA GGCGGGAGCC ACCACACCCG GCTATTTTTT TTTTTTTTTT  
6001 TTTNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNTTTTGG TAGAGACAGG  
6051 GTTTCACCAT GTTGCCAGG ATGGTCTCGA ACTCCTGACC TTGTGATCCA  
6101 CCCCCCGCCC CTCCCTCGGC CTTCCAAAGT GCTGGGATTA CAGGCGTGAG  
6151 CCACCACACC CAGCCTCCCC TAACCTTTTC TAAAGGACCC AGGAGTTTTG  
6201 AAGGATCCGG GAGTTCCTG TTCCTGAGC TGTGAATCAA CTGTGAAAT  
6251 CAAAGGCCAA GAGACTTATC ATGCTTTATA TAACATCTCT AGTGTTCCT

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6301 CCTGAGTTTC TTCTCTGAAG ACACATGTTT GGGAAACAAA ACTGTCCCTT  
 6351 TGAGATAAAA TCAAATAAGA AAATTGGATA ATAATCACAA CCTCAAAATG  
 6401 AGCTGGGGCC CATATGCTTG GGTGGCCGA ATGGAGTCAT GCCTGGAAGT  
 6451 GGAGGAGAGT GTCCAGGAGC TCCGATGACC CAAGGCATTT TAACCTTGGA  
 6501 ATCTGCTCTC CAGGCTACCA CCACATACCT CCCTCTTCCC CATTATCCCT  
 6551 GTGGCTTAGA AAAGAA (SEQ ID NO:3)

**FEATURES:**

Start: 2026  
 Exon: 2026-2224  
 Intron: 2225-2369  
 Exon: 2370-2513  
 Intron: 2514-3802  
 Exon: 3803-4540  
 Intron: 4541-5413  
 Exon: 5414-5703  
 Stop: 5704

**CHROMOSOME MAP POSITION:**

Chromosome 17

**ALLELIC VARIANTS (SNPs):**

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
423	G	A	Beyond ORF(5')			
2717	A	G	Intron			
3064	C	T	Intron			
4146	C	A	Exon	229	G	G
4440	T	C	Exon	327	S	S
4443	G	T	Exon	328	V	V
5105	T	C	Intron			

**Context:**

**DNA**

**Position**

423 TAATAAAGTCAAGATTGGAAGTGGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCAC  
 TTTGGGAGGCCAAGGCTGGTGGATCACTTGAGGTCAGGAGTTCGAGACCAGCGTGGCCAA  
 CATGGTGAGACCTCGTCTCTACTAAAAATACCAAAATTAAGTGGGCGTTGTGGTGGGAGC  
 CTGTAATCCCAGAACTCAGGAGACTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGA  
 GGTTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGCCACAGAGCAAGACTCC  
 [G,A]  
 TCTCAAAATAAATAAATAAATAAATAAATAAATAAAGACTGGAAGTGTGATCTGATTCT  
 AAAGACCCGAGTTCTTAATCACTATGTAATACAGCCACAGCAATTTCTGTATCTTTGGCA  
 TATTCACCCAGCCGACATTTTGAAGTATATATGTGTATTATTGATGATT  
 ACTTTTATTTCCACATATAAAATTATTTAAGGCTCAATATGTCTTTTAAGACTGCACAC  
 CTCCTCCCTGCCCTCACTTCTGTGTTGCTGCTTTCCCGAGTAATCTGGGAGTGAACATT

2717 GTGATGACTGGAGGCATCTTGCTGCGCTGGGGATGCTGCTCGCCTCTTTTGCTACTTCC  
 TTGACCCACCTATACCTGAGTATTGGGTTGCTGTCAGGTGAGAGCCTGCACAAGGGCAGG  
 AGAGTCAAATGCTTAGATCGTTGGATGTTACCTCCTTCCCTGCTCCTTCCAAAGGGTTTCG  
 GGGAGAAGCTGAGGGAAAGTTAGCTAGCACCTGTACCCAGAAGGGAATTCTTAATAGGA  
 ATGACTAAAGCGACAAACATGGTGAGGAATTAGGAAATTCAAGGATGATGAAACCTGGCC  
 [A,G]  
 GGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAAGCCGAGGCGGGTGGATCACG  
 AGGTCAGGAGTTTGGAGACCAGCTGGCCAACATGGTGAAACCCCGTCTTACAAAAATAC  
 AAAAATTAGCCGGGCTGGTGGCGCTAATCCAGTTACTCGGGAGGCTGAGGCAGGAGAA  
 TCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGCACCCTGCACTCCAGC  
 CTGGGCGACAGAGCAAGATTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGATGAA

3064 GCGGGTGGATCACGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCCGT  
CTCTACAAAAATACAAAAATTAGCCGGGCCTGGTGGCGCTAATCCCAGTTACTCGGGAGG  
CTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGCAC  
CACTGCACTCCAGCCTGGGCGACAGAGCAAGATTCTGTCTCAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGATGAAACCAAGTATACAAGCCCAGAACCTAGGGCTAATGGGACTGGAGTG  
[C, T]  
AAAAGGAAGAATTACTATAAAATGGTGCTAGGGGCCAGGCACGGTGGCTCACGCCTGTAA  
TCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACGAGGTCAGGAGATCAAGACCATCC  
TGGCTAACACGGTGAAATCACGTCTCTACTAAAAACACAAAAAATTAGCTGGGCGTGGTG  
GCAGGTGACTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGG  
GAAGCAGAGCTTGAGTGAGCCGAGATTGCACCACTGCACTCCAGCCTGGGCGACAGAGC

4146 GTCTGTTATTTCTCTCGCCGACGATCCCTGGCCACCGGGCTGGCACTGACAGGCGTGGG  
CCTCTCCTCCTTCACATTTGCCCCCTTTTTCAGTGGCTGCTCAGCCACTACGCCTGGAG  
GGGTCCCTGCTGCTGGTGTCTGCCCTCTCCCTCCACCTAGTGGCCTGTGGTGTCTCCT  
CCGCCCCACCTCCCTGGCTGAGGACCCTGCTGTGGGTGGTCCCAGGGCCCACTCACCTC  
TCTCCTCCATCATGGCCCCCTTCTCCGTTACACTGTTGCCCTCACCTGATCAACACTGG  
[C, A]  
TACTTCATTCCCTACCTCCACCTGGTGGCCCATCTCCAGGACCTGGATTGGGACCCACTA  
CCTGCTGCCTTCTACTCTCAGTTGTTGCTATTTCTGACCTCGTGGGGCGTGTGGTCTCC  
GGATGGCTGGGAGATGCAGTCCCAGGGCCTGTGACACGACTCCTGATGCTCTGGACCACC  
TTGACTGGGGTGTCACTAGCCCTGTTCCCTGTAGCTCAGGCTCCACAGCCCTGGTGGCT  
CTGGCTGTGGCCTACGGCTTACATCAGGGGCTCTGGCCCCACTGGCCTTCTCTGTGCTG

4440 CACTGGCTACTTCATTCCCTACCTCCACCTGGTGGCCCATCTCCAGGACCTGGATTGGGA  
CCCACTACCTGCTGCCTTCTACTCTCAGTTGTTGCTATTTCTGACCTCGTGGGGCGTGT  
GGTCTCCGGATGGCTGGGAGATGCAGTCCCAGGGCCTGTGACACGACTCCTGATGCTCTG  
GACCACCTTACTGGGGTGTCACTAGCCCTGTTCCCTGTAGCTCAGGCTCCACAGCCCT  
GGTGGCTCTGGCTGTGGCCTACGGCTTACATCAGGGGCTCTGGCCCCACTGGCCTTCTC  
[T, C]  
GTGCTGCCTGAACTAATAGGGACTAGAAGGATTTACTGTGGCCTGGGACTGTTGCAGATG  
ATAGAGAGCATCGGGGGGCTGCTGGGGCCTCCTCTCTCAGGTAAGTGGAATGGGGTTCCC  
AGGGGGTGAGGGTGCCATGTTGCACAAGTGGGGAGGGTACTATTCTCATTACAGTGTA  
TGTAATATTGCCCTCTGGTGTAGTACAGTACACAGCCTGCGTGGCCAACCATAGCATCC  
CTGAAATGGGTCCATGGGGCAAAGAACTTGGGGCTGGGAAAGTCTGAGTGGAAAGACAAA

4443 TGGCTACTTCATTCCCTACCTCCACCTGGTGGCCCATCTCCAGGACCTGGATTGGGACCC  
ACTACCTGCTGCCTTCTACTCTCAGTTGTTGCTATTTCTGACCTCGTGGGGCGTGTGGT  
CTCCGGATGGCTGGGAGATGCAGTCCCAGGGCCTGTGACACGACTCCTGATGCTCTGGAC  
CACCTTGACTGGGGTGTCACTAGCCCTGTTCCCTGTAGCTCAGGCTCCACAGCCCTGGT  
GGCTCTGGCTGTGGCCTACGGCTTACATCAGGGGCTCTGGCCCCACTGGCCTTCTCTGT  
[G, T]  
CTGCCTGAACTAATAGGGACTAGAAGGATTTACTGTGGCCTGGGACTGTTGCAGATGATA  
GAGAGCATCGGGGGGCTGCTGGGGCCTCCTCTCTCAGGTAAGTGGAATGGGGTTCCCAGG  
GGGTGAGGGCTGCCATGTTGCACAAGTGGGGAGGGTACTATTCTCATTACAGTGTATGT  
GAATATTGCCCTCTGGTGTAGTACAGTACACAGCCTGCGTGGCCAACCATAGCATCCCTG  
AAATGGGTCCATGGGGCAAAGAACTTGGGGCTGGGAAAGTCTGAGTGGAAAGACAAAAG

5105 CCTGGCCAGACACAGACGTAGCATTCCAGTGTGCACCCTTTCTTTGGCCTACTGGGCCC  
CAAACCAGGTATCTGAGGCACCTGGTCAAAGTTCTGCTGGCTCAGGGTGCCAGAACTTTC  
AGACCTTTATCTCCTCTTACCCATTAAGCTTTAGAAAGGCCACAGTTGGTGGGCG  
CCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCCGGGAGGCGG  
AGCTTGAGTGAGCTGAGATCGGCCACTGCACTTCAGCCTGGGCGACAGAGCGAGACTC  
[T, C]  
GTCTCAAAAAAAAAAAAAAAAAAGAAAGGCCACAGTTGCCAGAAAGAAAGGCACAAGTATGC  
CTGACTCAATCTGGATCTCCAAATCCCTGCAGGCTGGTTTGAGGTCTTTCTGAAGGCG  
GGGAGGTGGTTGAAATTAACTTTGGAGCCCTTTGGGAAACCAGAGTTCTTAAGTTTAT  
CCAATATTCCATGGGAGTTCCAATCCTCTGAGATGATAAGTCTTCCCTCCACCCAAAA  
ATGATCTGAGCCCTCAGCCCCAGCAAATAGATCACTCATGTGTATTCTTTTCTCTCTT

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